

C13
concl
sequence DVAQKLEQLE (SEQ ID NO:4), which immediately follows the 17 amino acid sequence underlined in Figure 3b.

Please replace the paragraph beginning at page 17, line 1, with the following rewritten paragraph:

C2
The present invention also extends to nucleic acid encoding *Rht* or a homologue obtainable using a nucleotide sequence derived from Figure 2 or Figure 3a, and such nucleic acid obtainable using one or more, e.g. a pair, of primers including a sequence shown in Table 1 (SEQ ID NO:21-SEQ ID NO:55).

Please replace the paragraph beginning at page 18, line 13, with the following rewritten paragraph:

C3
Some preferred embodiments of polypeptides according to the present invention (encoded by nucleic acid embodiments according to the present invention) include the 17 amino acid sequence which is underlined in Figure 3b, or a contiguous sequence of amino acids residues with at least about 10 residues with similarity or identity with the respective corresponding residue (in terms of position) in 17 amino acids which are underlined in Figure 3b, more preferably 11, 12, 13, 14, 15, 16 or 17 such residues,

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could

and/or the sequence DVAQKLEQLE, or a contiguous sequence of amino acids with at least about 5 residues with similarity or identity with the respective corresponding residue (in terms of position) within DVAQKLEQLE, more preferably 6, 7, 8 or 9 such residues. Further embodiments include the 27 amino acid sequence DELLAALGYKVRASDMADVAQKLEQLE (SEQ ID NO:56), or a contiguous sequence of amino acids residues with at least about 15 residues with similarity or identity with the respective corresponding residue (in terms of position) within this sequence, more preferably 16, 17, 18, 19, 20, 21, 22, 23, 24, 25 or 26 such residues.

Please replace the paragraph beginning at page 41, line 25, with the following rewritten paragraph:

C4

Figure 1: Alignment of N-terminus predicted GAI amino acid sequence (Gai) (SEQ ID NO:78) with rice EST D39460 (0830) (SEQ ID NO:79), with a region of homology outlined in black.

Please replace the paragraph beginning at page 42, line 3, with the following rewritten paragraph:

C5

Figure 2a shows a consensus DNA sequence cDNA C15-1 (obtained via single-pass sequencing) (SEQ ID NO:57).

Please replace the paragraph beginning at page 42,
line 6, with the following rewritten paragraph:

CO Figure 2b shows data from original DNA sequencing runs
from 14a1 (single-pass) (SEQ ID NO:58-SEQ ID NO:70).

Please replace the paragraph beginning at page 42,
line 9, with the following rewritten paragraph:

CA Figure 2c shows data from original DNA sequencing runs
from 5a1 (single-pass) (SEQ ID NO:71-SEQ ID NO:77).

Please replace the paragraph beginning at page 42,
line 14, with the following rewritten paragraph:

CB Figure 3a shows a composite DNA sequence of wheat *Rht*
gene derived from data in Figure 2, including coding
sequence (SEQ ID NO:3).

Please replace the paragraph beginning at page 42,
line 17, with the following rewritten paragraph:

CA Figure 3b shows an alignment of the entire predicted
Rht protein sequence encoded by the coding sequence of
Figure 2 (*rht*) with the entire predicted *GAI* protein
sequence of *Arabidopsis* (*Gai*) (SEQ ID NO:1 and SEQ ID

CP could
NO:2). Regions of sequence identity are highlighted in black.

Please replace the paragraph beginning at page 42, line 25, with the following rewritten paragraph:

CP
Figure 4a shows DNA sequence (single-pass) of rice cDNA D39460 (SEQ ID NO:19). This cDNA is an incomplete, partial clone, missing the 3' end of the mRNA from which it is derived.

Please replace the paragraph beginning at page 43, line 1, with the following rewritten paragraph:

CP
Figure 4b shows alignment of the entire predicted Rht protein sequence (wheat - encoded by the coding sequence of Figure 2) with that of GAI (Gai) and rice protein sequence predicted from DNA sequence in Figure 4a (Rice) (SEQ ID NO:20). Regions of amino acid identity are highlighted in black; some conservative substitutions are shaded.

Please replace the paragraph beginning at page 43, line 12, with the following rewritten paragraph:

C12
Figure 6a shows the nucleotide sequence of rice EST
D39460, as determined by the present inventors (SEQ ID
NO:12).

Please replace the paragraph beginning at page 43,
line 15, with the following rewritten paragraph:

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Figure 6b shows the predicted amino acid sequence (SEQ
ID NO:5) encoded by the rice EST sequence of Figure 6a.

Please replace the paragraph beginning at page 43,
line 20, with the following rewritten paragraph:

C14
Figure 7a shows the nucleotide sequence of the wheat
C15-1 cDNA (SEQ ID NO:13).

Please replace the paragraph beginning at page 43,
line 23, with the following rewritten paragraph:

C15
Figure 7b shows the predicted amino acid sequence (SEQ
ID NO:6) of the wheat C15-1 cDNA of Figure 7a.

Please replace the paragraph beginning at page 43,
line 28, with the following rewritten paragraph:

C16
Figure 8a shows the nucleotide sequence of the 5a1 wheat genomic clone (SEQ ID NO:14).

Please replace the paragraph beginning at page 44, line 3, with the following rewritten paragraph:

C17
Figure 8b shows the predicted amino acid sequence (SEQ ID NO:7) of the 5a1 wheat genomic clone of Figure 8a.

Please replace the paragraph beginning at page 44, line 8, with the following rewritten paragraph:

C18
Figure 9a shows the nucleotide sequence of the 1a1 maize genomic clone, i.e. D8 (SEQ ID NO:15).

Please replace the paragraph beginning at page 44, line 11, with the following rewritten paragraph:

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Figure 9b shows the amino acid sequence (SEQ ID NO:8) of the maize 1a1 genomic clone of Figure 9a.

Please replace the paragraph beginning at page 44, line 21, with the following rewritten paragraph:

C20 Figure 11a shows a partial nucleotide sequence of the maize-D8-1 allele (SEQ ID NO:16).

Please replace the paragraph beginning at page 44, line 24, with the following rewritten paragraph:

C21 Figure 11b shows a partial amino acid sequence (SEQ ID NO:9) of the maize D8-1 allele.

Please replace the paragraph beginning at page 44, line 27, with the following rewritten paragraph:

C22 Figure 11c shows a partial nucleotide sequence of the maize D8-2023 allele (SEQ ID NO:17).

Please replace the paragraph beginning at page 45, line 1, with the following rewritten paragraph:

C23 Figure 11d shows a partial amino acid sequence (SEQ ID NO:10) of the maize D8-2023 allele.

Please replace the paragraph beginning at page 45, line 6, with the following rewritten paragraph:

C24
Figure 12a shows a partial nucleotide sequence of the wheat *rht-10* allele (SEQ ID NO:18).

Please replace the paragraph beginning at page 45, line 9, with the following rewritten paragraph:

C25
Figure 12b shows a partial amino acid sequence (SEQ ID NO:11) of the wheat *rht-10* allele.

Please replace the paragraph beginning at page 45, line 23, with the following rewritten paragraph:

C24
Previously, we cloned the *GAI* gene of *Arabidopsis* (PCT/GB97/00390 - WO97/29123 published 14 August 1997). Comparison of the DNA sequences of the wild-type (*GAI*) and mutant (*gai*) alleles showed that *gai* encodes a mutant predicted protein product (*gai*) which lacks a segment of 17 amino acids from close to the N-terminus of the protein. Screening of the DNA sequence databases with the *GAI* sequence revealed the existence of a rice EST (D39460) which contains a region of sequence very closely related to that of the segment that is deleted from *GAI* in the *gai* protein. A comparison of the predicted amino acid sequences from the region DELLA (SEQ ID NO:107) to EQLE (SEQ ID NO:108) are identical in both sequences. The two

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conserved

differences (V/A; E/D) are conservative substitutions, in which one amino acid residue is replaced by another having very similar chemical properties. In addition, the region of identity extends beyond the boundary of the deletion region in the gai protein. The sequence DVAQKLEQLE is not affected by the deletion in gai, and yet is perfectly conserved between the GAI and D39460 sequences (Figure 1).

Please replace the paragraph beginning at page 49, line 20, with the following rewritten paragraph:

C27

Mutations were found in the candidate *D8* and *Rht* genes in each of the above mutants. The *D8*-1 mutation is an in-frame deletion which removes amino acids VAQK (SEQ ID NO:101) (55-59) and adds a G (see sequence in Figure 11a and Figure 11b). This deletion overlaps with the conserved DVAQKLEQLE homology block described above. *D8*-2023 is another in-frame deletion mutation that removes amino acids LATDTVHYNPSD (SEQ ID NO:102) (87-98) from the N-terminus of the *D8* protein (see Figure 11c and Figure 11d). This deletion does not overlap with the deletion in *gai* or *D8*-1, but covers another region that is highly conserved between *GAI*, *D8* and *Rht* (see Figure 10). Finally, *Rht*-*D1c* contains another small in-frame deletion that removes amino acids

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could

LNAPPPPLPPAPQ (SEQ ID NO:103) (109-121) in the N-terminal region of the mutant Rht protein that it encodes (see Figure 12a and Figure 12b) (LN-P is conserved between GAI, D8 and Rht, see Figure 10).

Please replace the paragraph beginning at page 52, line 1, with the following rewritten paragraph:

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TABLE 2 - Primers used in the sequence of D-8 clones (SEQ ID NO:80-SEQ ID NO:100)

IN THE CLAIMS:

Please substitute the following amended claims for corresponding claims previously presented. A copy of the amended claims showing current revisions is attached.

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1. (Amended) An isolated polynucleotide encoding a polypeptide which comprises the amino acid sequence DELLAALGYKVRASDMA (SEQ ID NO:104) and which on expression in a *Triticum Aestivum* plant provides inhibition of growth of the plant, which inhibition is antagonised by gibberellin.
